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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2009; month=8; day=7; hr=14; min=1; sec=32; ms=695; ]

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Application No: 10583785 Version No: 4.0

**Input Set:****Output Set:**

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**Finished:** 2009-07-31 15:25:18.514  
**Elapsed:** 0 hr(s) 0 min(s) 15 sec(s) 76 ms  
**Total Warnings:** 22  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 40  
**Actual SeqID Count:** 40

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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (25)
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W 213	Artificial or Unknown found in <213> in SEQ ID (38)

**Input Set:**

**Output Set:**

**Started:** 2009-07-31 15:25:03.438  
**Finished:** 2009-07-31 15:25:18.514  
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**Total Warnings:** 22  
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**No. of SeqIDs Defined:** 40  
**Actual SeqID Count:** 40

**Error code**

**Error Description**

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SEQUENCE LISTING

<110> SEEGER, WERNER  
GUNTHER, ANDREAS  
RUPPERT, CLEMENS  
MARKART, PHILIPP  
MAGDOLEN, VIKTOR  
WEAVER, TIMOTHY E.

<120> NOVEL CHIMERIC PLASMINOGEN ACTIVATORS AND THEIR PHARMACEUTICAL  
USE

<130> VJP-1050-US

<140> 10583785  
<141> 2009-07-31

<150> PCT/EP2003/014542  
<151> 2003-12-18

<160> 40

<170> PatentIn version 3.5

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<211> 1143  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(1143)  
<223> Coding sequence of the surfactant protein B precursor

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1 5 10 15  
  
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30  
  
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45  
  
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60  
  
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

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Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
 aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
 aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
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 tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
 ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
 gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
 aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
 tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
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Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
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245 250 255	
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Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
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Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro	
275 280 285	
 aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc	912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser	
290 295 300	
 gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca	960

Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala  
305 310 315 320

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Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys  
325 330 335

caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg 1056  
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg  
340 345 350

ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc 1104  
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr  
355 360 365

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<211> 837  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(837)  
<223> Coding sequence of the surfactant protein B precursor lacking  
the C-terminal propeptide

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1 5 10 15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt 96  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag 144  
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga 192  
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac 240  
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg 288  
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
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Leu Val Leu Arg Cys Ser Met	
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 <213> Homo sapiens

<220>  
 <221> CDS

<222> (1)..(237)

<223> Coding sequence of the mature surfactant protein B

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cgg	atc	caa	gcc	atg	att	ccc	aag	ggg	gcg	cta	gct	gtg	gca	gtg	gcc	96
Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	
		20						25					30			

cag	gtg	tgc	cgc	gtg	gta	cct	ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	144
Gln	Val	Cys	Arg	Val	Val	Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	
		35					40					45				

ctg	gct	gag	cgc	tac	tcc	gtc	atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	192
Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	
	50					55				60						

atg	ctg	ccc	cag	ctg	gtc	tgc	cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg	237
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<211> 1293

<212> DNA

<213> Homo sapiens

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<222> (1)..(1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

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1				5					10					15		

gac	tcc	aaa	ggc	agc	aat	gaa	ctt	cat	caa	gtt	cca	tcg	aac	tgt	gac	96
Asp	Ser	Lys	Gly	Ser	Asn	Glu	Leu	His	Gln	Val	Pro	Ser	Asn	Cys	Asp	
		20						25					30			

tgt	cta	aat	gga	gga	aca	tgt	gtg	tcc	aac	aag	tac	ttc	tcc	aac	att	144
Cys	Leu	Asn	Gly	Gly	Thr	Cys	Val	Ser	Asn	Lys	Tyr	Phe	Ser	Asn	Ile	
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cac	tgg	tgc	aac	tgc	cca	aag	aaa	ttc	gga	ggg	cag	cac	tgt	gaa	ata	192
His	Trp	Cys	Asn	Cys	Pro	Lys	Lys	Phe	Gly	Gly	Gln	His	Cys	Glu	Ile	
	50					55					60					

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Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
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Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
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gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val	
195 200 205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His	
210 215 220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly	
225 230 235 240	
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val	
245 250 255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac	816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His	
260 265 270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys	
275 280 285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat	912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr	
290 295 300	

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	370					375					380					
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Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
385					390					395					400	
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Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	S				